AMENDMENTS TO THE CLAIMS

1. – 46. (Canceled)

47. (New) A method of producing L-glutamic acid, comprising:

culturing a coryneform bacterium expressing an enzyme encoded by a coryneform bacteria glutamic acid biosynthesizing gene, in a medium for a time and under conditions suitable to produce and accumulate said L-glutamic acid in the medium, and

collecting said L-glutamic acid from the medium;

wherein the glutamic acid biosynthesizing gene is located on a chromosome of the coryneform bacterium and the enzyme is selected from the group consisting of glutamate dehydrogenase, citrate synthase, isocitrate dehydrogenase, pyruvate dehydrogenase, and aconitase, said glutamic acid biosynthesizing gene comprising a DNA sequence situated at about position -35 from the transcription start site of the glutamic acid biosynthesizing gene, wherein said DNA sequence is selected from the group consisting of TTGTCA and TTGCCA,

wherein said producing L-glutamic acid is at a level greater than the production of L-glutamic acid by the corresponding wild-type coryneform bacterium.

48. (New) The method of claim 47, wherein said glutamic acid biosynthesizing gene encodes glutamate dehydrogenase.

49. (New) The method of claim 47, wherein said glutamic acid biosynthesizing gene encodes citrate synthase.

50. (New) The method of claim 47, wherein said glutamic acid biosynthesizing gene encodes isocitrate dehydrogenase.

51. (New) The method of claim 47, wherein said glutamic acid biosynthesizing gene encodes pyruvate dehydrogenase.

52. (New) The method of claim 47, wherein said glutamic acid biosynthesizing gene encodes aconitase.

53. (New) The method of claim 47, wherein said DNA sequence situated at about position -35 from the transcription start site of the glutamic acid biosynthesizing gene further comprises TATAAT situated at about position -10 from the transcription start site.

54. (New) The method of claim 47, wherein said DNA sequence is TTGTCA.

55. (New) The method of claim 54, wherein said glutamic acid biosynthesizing gene further comprises TATAAT situated at about position -10 from the transcription start site of the gene.

56. (New) The method of claim 54, wherein said glutamic acid biosynthesizing gene further comprises TATAAC situated at about position -10 from the transcription start site of the gene.

57. (New) The method of claim 47, wherein said DNA sequence is TTGCCA.

58. (New) The method of claim 57, wherein said glutamic acid biosynthesizing gene further comprises TATAAT situated at about position -10 from the transcription start site of the gene.

59. (New) The method of claim 57, wherein said glutamic acid biosynthesizing gene further comprises TATAAC situated at about position -10 from the transcription start site of the gene.

60. (New) The method of claim 47, wherein said glutamic acid biosynthesizing gene encodes isocitrate dehydrogenase and wherein said DNA sequence is TTGCCA.

61. (New) The method of claim 60, wherein said glutamic acid biosynthesizing gene further comprises TATAAT situated at about position -10 from the transcription site of the gene.

62. (New) The method of claim 47, wherein said glutamic acid biosynthesizing gene encodes pyruvate dehydrogenase and wherein said DNA sequence is TTGCCA.

63. (New) The method of claim 62, wherein said glutamic acid biosynthesizing gene further comprises TATAAT situated at about position -10 from the transcription site of the gene.

64. (New) A method of producing L-glutamic acid, comprising:

culturing a coryneform bacterium expressing an enzyme encoded by a coryneform bacteria glutamic acid biosynthesizing gene, in a medium for a time and under conditions suitable to produce and accumulate said L-glutamic acid in the medium, and

collecting said L-glutamic acid from the medium;

wherein the glutamic acid biosynthesizing gene is located on a chromosome of the coryneform bacterium and the enzyme is selected from the group consisting of glutamate dehydrogenase, citrate synthase, isocitrate dehydrogenase, pyruvate dehydrogenase, and aconitase, said glutamic acid biosynthesizing gene comprising a DNA sequence situated at about position -10 from the transcription start site of the glutamic acid biosynthesizing gene, wherein said DNA sequence is TATAAC,

wherein said producing L-glutamic acid is at a level greater than the production of L-glutamic acid by the corresponding wild-type coryneform bacterium.

65. (New) The method of claim 64, wherein said glutamic acid biosynthesizing gene encodes glutamate dehydrogenase.

66. (New) The method of claim 64, wherein said glutamic acid biosynthesizing gene encodes citrate synthase.

67. (New) The method of claim 66, wherein said glutamic acid biosynthesizing gene further comprises TTGACA situated at about position -35 from the transcription start site of the gene.

68. (New) The method of claim 64, wherein said glutamic acid biosynthesizing gene encodes isocitrate dehydrogenase.

69. (New) The method of claim 68, wherein said glutamic acid biosynthesizing gene further comprises TTGACA situated at about position -35 from the transcription start site of the gene.

70. (New) The method of claim 64, wherein said glutamic acid biosynthesizing gene encodes pyruvate dehydrogenase.

71. (New) The method of claim 64, wherein said glutamic acid biosynthesizing gene encodes aconitase.

72. (New) The method of Claim 64, wherein said glutamic acid biosynthesizing gene further comprises TTGACA situated at about position -35 from the transcription site of the gene.

SUPPORT FOR THE AMENDMENTS

Claims 1-19 were previously canceled.

Claims 20-46 are presently canceled.

Claims 47-72 have been added.

New Claims 47-72 are supported by the originally, pending claims, the previously pending claims, and the specification as originally filed, for example, page 3, lines 7-10, page 4, line 23 to page 5, line 3, page 9, lines 10-24, page 10, lines 5-7 and lines 17-12, page 10, line 25 to page 12, line 8, the Examples, and Table 17 (page 20).

No new matter has been entered by the present amendment.